

Freeze/Thaw Sample Sequence

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GCCAGATCAGACCTTTAGTCTGAACCGGGATCTTACAGGAGAATTAGAGTATGCTACAAA HUM-UC331 CTCTGAGATGAGACTGTACAAGAATATTCCACAGATGTCCTTTGATGATACAGAAAGGGA HUM-UC331 CTCGGAGATGAGACTGTACAAGAACATTCCACAGATGTCATTTGATGACACAGAAAGGGA MOU-UC331 GCCAGAGCAGACCTTCAGTCTGAACCGAGACATTACAGGAGAATTAGAATATGCTACGAA MOU-UC331 540 480 450 510

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069

720

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GGTTACCCCACACACACTTTATTTCCTAAGGGCTGGCCAAGGCTCCCATAGAGGCGCT HUM-UC331 MOU-UC331 GGTCACCCCGCAGACACACTTCATTTCTTAAGGGCCAGCCGGGGCTCCCTCAGATGCGCT *

750

840 AAAGGGATGAGGCTCCAGAGAG HUM-UC331 AGAGG-ATGCTCCAGCAAT MOU-UC331 * * * * * * *	900 GCTTGCTGCAGAAACCTGGCC HUM-UC331 GG-TTGCTGCAGGAACCTGGCC MOU-UC331	960 GCCAGGGGACCATCGTGGTTCT HUM-UC331 GCCAAGGGATAGTCTCTCT MOU-UC331	1020 ATCTGGCAGTCATGGGTAACAC HUM-UC331 ATCTGTCAGTCATGAATAATGC MOU-UC331	1080 FCATGTTGCTTTGTGGAAGATT HUM-UC331 FCTTTTTGCTT-GATTTCTTGT MOU-UC331	1140 PTTGTTTTTAAAGGAAACTATTTGTGGGC HUM-UC331TCAAAAAGGATGCTTCCTTGACCG MOU-UC331 ****** ***
840 GTGTCAGTGAAGATGTACGACTACCTGTTGGGAAGGACAAAGGGATGAGGCTCCAGAGAG GTTAGTGAAGATGTGCGACCACCTGCTGGGAAGGACAAGAGGACATGCTCCAGCAAT **** **** ****	AGTIGGCIGCCACAGCICITIGICTITIGGGGCTIGCAGAAACCIGGCC AGTIGCCIGCCAGAGCTITIGIC-ICGGGG-IIGCIGCAGGAACCIGGCC * * * * * * * * * * * * * * * * * *	930 TACGGAAGATACGACACCACTGGGAGGGTTGTGTGTGTGCCAGGGGACCATCGTGGTTCT TGTGGAAACCGCCTCACCACCAGGAGCGGTATGGGTGCCAAGGGATAGTCTCTCT ** *** ** ** ** ** ***	1020 CTAGGGCGCTGTGGAAATTGGGTCTTGGGTTGGGTTGGCATCTGGCTAGTTAACAC CTAAGGCACTGCAGAAACTGGGTCTTTAGGCTTGGGTTGGCATCTGTCAGTCA	1050 TTGCTTTTCCAGTTAATGTGGCCATGTGATTCCAAGTGTCATGTTGCTTTGTGGAAGATT TCACTT-CCCAGTC-TGTGGCCACGGGATCCCATGTGTTTTTTGCTT-GATTTCTTGT ** ** ** ** ** ** ** ** ** ** ** ** **	1110 GTTGTGTGACTTGTTTTTTGATTTTGTATTTTGTTTTTTAAAGGAAACTATTTGTGGGC GTGGTTTGTCCT-TTTGTGGCATCAAAAAGGATGCTTCCTTGACCG * * * * * * * * * * * * * * * * * * *

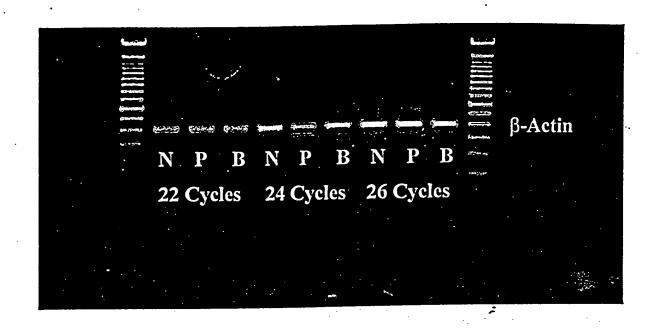
1170 TATAGGAAACTTTCTGATGCCTCCGGATT-GTGTTAGTAGTAGCCATCAGGAGGGTCTCC TAGAATCCTTCTGAAACCCG-AGTTTCGTGTTTTGAATTAGCCATCAGGAGGGTCTCC * **** * * * * * * * * * * * * * * *	1200 AGTAGCCATCAGGAGGGTCTCC ATTAGCCATCAGGAGGGTCTCC **	HUM-UC331 MOU-UC331
AACTA-AAACACTT-GTTCCTGCTTGCTCCTTTTCCCCTCTCATTGTTCAGCATTCTTGTC AGCTAGAAACACTTCGTCCTTGCTCCT-CCTCTCTTGTCAGCATTCGTGTC * * * * * * * * * * * * * * * * * * *	1260 CTCATTGTTCAGCATTCTTGTC GTCATTGCTCAGCATTCGTGTC *	HUM-UC331 MOU-UC331
AAGTTGCCCAGCTTGGAGTTGTCTGTCACGCACATGTGTCCTGTGGTTATAGCTAGAAGGAGGTGCCTAGCTAG	1320 TCCTGTGGTTATAGCTAGAAGG TCCCACAATGGTGGTTGGAAAG	HUM-UC331 MOU-UC331
ACAGGAGTCTCCTGCTGATGCGTGATAGCTTAAGCTTGGGGAGAAGGTCTTTTCCACTGCGAAGGACTCTTTTCCACTGCGAAGGACTCTTTTCCACTGCACAAGGAAGG	1380 GGGAGAAGGTCTTTTCCACTGC GGGAAGG-CTTACACAGT-C	HUM-UC331 MOU-UC331
1410 CTAGCTAAGCAGTCTGGGGAGCATGGGGATCATTTCTATGTGTGTG	1410 rggggatCatttCtatgtGtGtGgtAatCtGGtC TCCTTTCCCTGTGTGGGTGACCTGGTT ****** * * * * * * * * * * * * * * * *	HUM-UC331 MOU-UC331
1470 AGTAAGATTGAGACTTAGTTAAGATTCCCCTTGGAAATTCCTTAATGTTTATTAGCTT GGGGTAAAAACTGAGACAGTAAAGATTCCTCTTGGGACCTCCTTGGTGTTTCCTTGCTT * ** * * * * * * * * * * * * * * * *	1500 ATTCCTTAATGTTTATTAGCTT CCTCCTTGGTGTTTCCCTGCTT ** ***	HUM-UC331 MOU-UC331

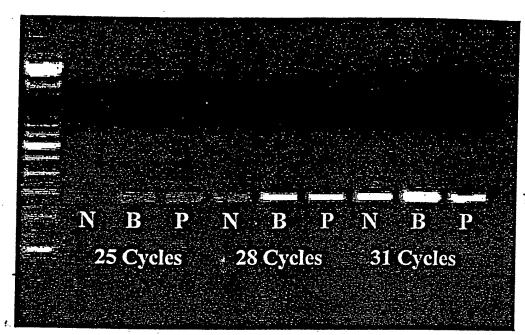
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1530	CTAACTAGTGTTGTAAGTCCGATGCCAGAATTTGGAGATTTGAGTTCTTTTTTTT	CTAACTCATGTTATAAACCCAGGGCTGGAGTCTGGAGACCCTGCTCCTTCTGTTCATGGC MOU-UC331	* * ***** * * ** ** ** * * *	1590	TTTTATTCACTGTGACTAATAAGCTTCCTAATAAATCCTTGCCAGACTTAAAAAAAA	TTTCATTCATGGTGACTAATGAGCTTCCTAATAAATCCTTAG-AGACTTAAAA	* * *

30 40 10 20 MSHGHSHGGGGCRCAAER-EEPPEORGLAYGLYLRIDLE HUM-UC331 >CSHGHSHN-----CAAEHIPEVPGDDVYRYDMVSYIDME ZK353.1 50 70 80 60 RLOCLNESREGSGRGVFKPWEERTDRSKFIESDADEELLF HUM-UC331 >FKPWEERTDRSKFAESDADEELLF MOU-UC331 KVTTLNESVDGAGKKVFKVMEKRDDRLEYVESDCDHELLF ZK353.1 90 120 100 110 NIPFTGNVKLKGIIIMGEDDDSHPSEMRLYKNIPOMSFDD HUM-UC331 NIPFTCNVKLKGVIIMGEDDDSHPSEMRLYKNIPOMSFDD MOU-UC331 NTPFTGHVRLTGLSITGDEDGSHPAKIRLFKDREAMSFDD ZK353.1 140 150 160 130 TEREPDOTFSLNRDLTGELEYATKISRFSNVYHLSIHISK HUM-UC331 TEREPEOTFSLNRDITGELEYATKISRFSNVYHLSIHISK MOU-UC331 CSIEADQEIDLKQDPQGLVDYPLKASKFGNIHNLSILVDA ZK353.1 200 170 180 190 NFGADTTKVFYIGLRGEWTELRRHEVTICNYEASANPADH HUM-UC331 NFGADTTKIFYIGLRGEWTELRRHEVTICNYEASANPADH MOU-UC331 NFGEDETKIYYIGLRGEFOHEFRORIAIATYESRAQLKDH ZK353.1

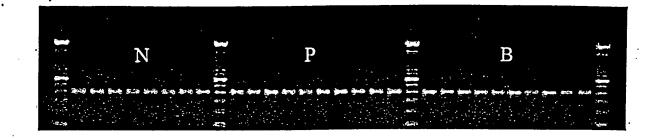
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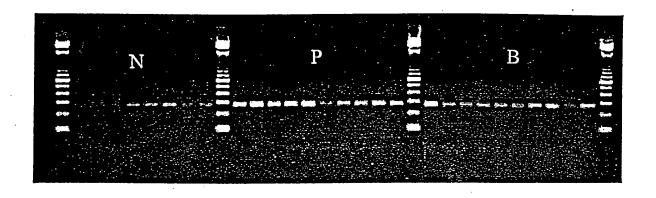
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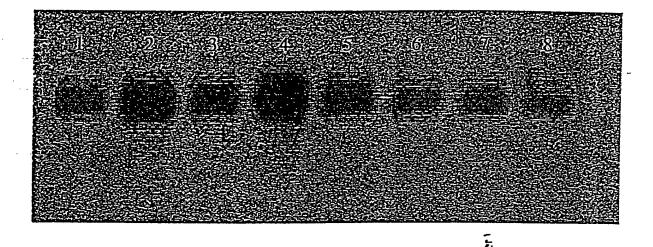




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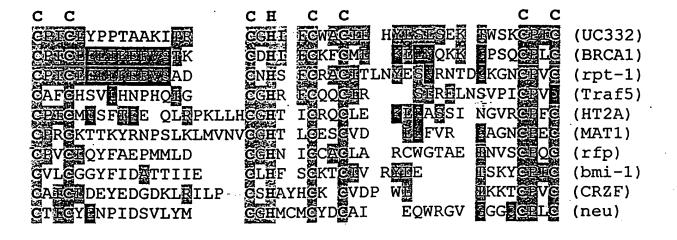


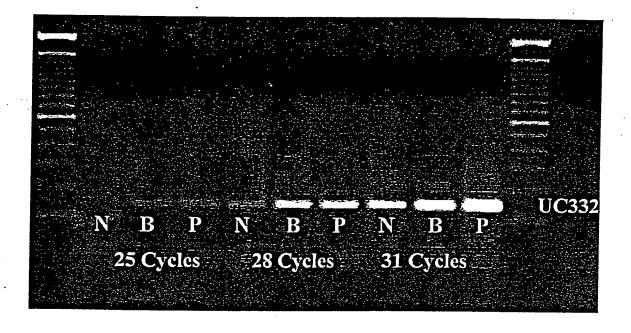
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110	120			150	
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160	170			200	
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660 AGTAAGGCCA ATG ATG GAT	670 TATGTTGCCC GGA AAG A	680 CTCTGGAGGT AC TCC AGT	690 GCTTGTCAAC GGA TCC AAG	698 TACTCTGG	740 14
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AGTAAGGCCA ATG ATG GATMET MET AGT AST Lys MET AAC CAG TCC AST GIN Ser AAC AAG ATC AST Lys MET TTT AGC TCT Phe Ser Ser GAG GCT CAA GIU Ala GIT CCT AAG AAC Pro Lys Lys GAA CCC CGT	TATGTTGCCC TATGTTGCCCC TATGTTGCCCCCCCCCC	CTCTGGAGGT AC TCC AGT Sn Ser Ser CC TAC CCC er Tyr Pro CC AGT TCA er Ser Ser AA AGG GGC In Arg Gly AT GGT GGA Sn Gly Gly AG TTT AGC Lu Phe Ser TG AAC CAC eu Asn His CG GGT CAC	GGA TCC AAG GLY Ser Lys AAA AAT GAA Lys Asn Glu CAG AAA AGC Gln Lys Ser GGC GGC AGC GLY GLY Ser AGA CGA GAT Arg Arg Asp CCT GCC CAG Pro Ala Gln ITG TTG AAT Leu Leu Asn	TACTCTGG CGT TAT AAT ATG Tyr Asn AGT TTT AAC Ser Phe Asn AGC AAA CTC Ser Lys Leu GAG GTA GCA Glu Val Ala TTC TCT GGT Phe Ser Gly TTC ACT TTT	782 28 824 42 866 56 908 70 950 84 992 98

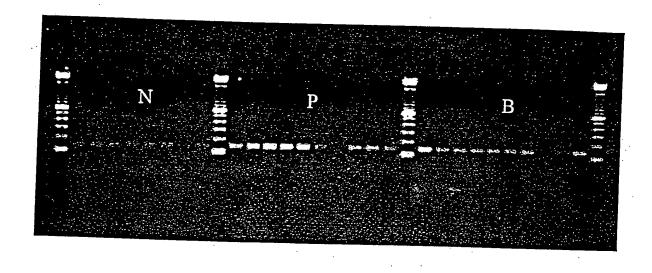
GGT AGC TGG GGA GG AGG AAC AAG TGG GGA CAT A CCT TTT 1076 Gly Ser Trp Gly Lys Arg Asn Lys Trp Gly His Lys Pro Phe 126 AAC AAG GAA CTC TTT TTA CAG GCC AAC TGC CAA TTT GTG GTG 1118 Asn Lys Glu Leu Phe Leu Gln Ala Asn Cys Gln Phe Val Val 140 TCT GAA GAC CAA GAC TAC ACA GCT CAT TTT GCT GAT CCT GAT 1160 Ser Glu Asp Gln Asp Tyr Thr Ala His Phe Ala Asp Pro Asp 154 ACA TTA GTT AAC TGG GAC TTT GTG GAA CAA GTG CGC ATT TGT 1202 Thr Leu Val Asn Trp Asp Phe Val Glu Gln Val Arg Ile Cys 168 AGC CAT GAA GTG CCA TCT TGC CCA ATA TGC CTC TAT CCA CCT 1244 Ser His Glu Val Pro Ser System Te Cystem 182 ACT GCA GCC AAG ATA ACC CGT TGT GGA CAC ATC TTC TGC TGG 1286 The Dis Alice we have the Property of the line and the Cystline 196 GCA TGC ATC CTG CAC TAT CTT TCA CTG AGT GAG AAG ACG TGG 1328 TO GVE THE THE TWELET SET TO BE THE THE 210 AGT AAA TGT CCC ATC TGT TAC AGT TCT GTG CAT AAG AAG GAT 1370 Tyr Ser Val His Lys Lys Asp 224 CTC AAG AGT GTT GTT GCC ACA GAG TCA CAT CAG TAT GTT GTT 1412 Leu Lys Ser Val Val Ala Thr Glu Ser His Gln Tyr Val Val 238 GGT GAT ACC ATT ACG ATG CAG CTG ATG AAG AGG GAG AAA GGG 1454 Gly Asp Thr Ile Thr Met Gln Leu Met Lys Arg Glu Lys Gly 252 GTG TTG GTG GCT TTG CCC AAA TCC AAA TGG ATG AAT GTA GAC 1496 Val Leu Val Ala Leu Pro Lys Ser Lys Trp Met Asn Val Asp 266 CAT CCC ATT CAT CTA GGA GAT GAA CAG CAC AGC CAG TAC TCC 1538 His Pro Ile His Leu Gly Asp Glu Gln His Ser Gln Tyr Ser 280 AAG TTG CTG CTG GCC TCT AAG GAG CAG GTG CTG CAC CGG GTA 1580 Lys Leu Leu Ala Ser Lys Glu Gln Val Leu His Arg Val 294 GTT CTG GAG GAG AAA GTA GCA CTA GAG CAG CAG CTG GCA GAG 1622 Val Leu Glu Glu Lys Val Ala Leu Glu Gln Gln Leu Ala Glu 308 GAG AAG CAC ACT CCC GAG TCC TGC TTT ATT GAG GCA GCT ATC 1664 Glu Lys His Thr Pro Glu Ser Cys Phe Ile Glu Ala Ala Ile 322 CAG GAG CTC AAG ACT CGG GAA GAG GCT CTG TCG GGA TTG GCC 1706 Gln Glu Leu Lys Thr Arg Glu Glu Ala Leu Ser Gly Leu Ala 336 GGA AGC AGA AGG GAG GTC ACT GGT GTT GTG GCT CTG GAA 1748 Gly Ser Arg Arg Glu Val Thr Gly Val Val Ala Ala Leu Glu 350

CAA CTG GTG CT GCT CCC TTG GCG AAG GAG GTT TTT 1790 Gln Leu Val Leu Met Ala Pro Leu Ala Lys Glu Ser Val Phe 364 CAA CCC AGG AAG GGT GTG CTG GAG TAT CTG TCT GCC TTC GAT 1832 Gln Pro Arg Lys Gly Val Leu Glu Tyr Leu Ser Ala Phe Asp 378 GAA GAA ACC ACG GAA GTT TGT TCT CTG GAC ACT CCT TCT AGA 1874 Glu Glu Thr Thr Glu Val Cys Ser Leu Asp Thr Pro Ser Arg 392 CCT CTT GCT CTC CCT CTG GTA GAA GAG GAG GAA GCA GTG TCT 1916 Pro Leu Ala Leu Pro Leu Val Glu Glu Glu Ala Val Ser 406 GAA CCA GAG CCT GAG GGG TTG CCA GAG GCC TGT GAT GAC TTG 1958 Glu Pro Glu Pro Glu Gly Leu Pro Glu Ala Cys Asp Asp Leu 420 GAG TTA GCA GAT GAC AAT CTT AAA GAG GGG ACC ATT TGC ACT 2000 Glu Leu Ala Asp Asp Asn Leu Lys Glu Gly Thr Ile Cys Thr 434 GAG TCC AGC CAG CAG GAA CCC ATC ACC AAG TCA GGC TTC ACA 2042 Glu Ser Ser Gln Gln Glu Pro Ile Thr Lys Ser Gly Phe Thr 448 CGC CTC AGC AGC TCT CCT TGT TAC TAC TTT TAC CAA GCG GAA 2084 Arg Leu Ser Ser Pro Cys Tyr Tyr Phe Tyr Gln Ala Glu 462 GAT GGA CAG CAT ATG TTC CTG CAC CCT GTG AAT GTG CGC TGC 2126 Asp Gly Gln His Met Phe Leu His Pro Val Asn Val Arg Cys 476 CTC GTG CGG GAG TAC GGC AGC CTG GAG AGG AGC CCC GAG AAG 2168 Petry Walt Visco Celent Myse City Selection Yellow Acting Select Prior City Myse 490 ATC TCA GCA ACT GTG GTG GAG ATT GCT GGC TAC TCC ATG TCT 2210 Me Ser Alta Bha Wall Male Columbia Ala Gly Tyr Ser Met Ser 504 GAG GAT GTT CGA CAG CGT CAC AGA TAT CTC TCT CAC TTG CCA 2252 Glu Asp Val Arg Gln Arg His Arg Tyr Leu Ser His Leu Pro 518 CTC ACC TGT GAG TTC AGC ATC TGT GAA CTG GCT TTG CAA CCT 2294 Leu Thr Cys Glu Phe Ser Ile Cys Glu Leu Ala Leu Gln Pro 532 CCT GTG GTC TCT AAG GAA ACC CTA GAG ATG TTC TCA GAT GAC 2336 Pro Val Val Ser Lys Glu Thr Leu Glu Met Phe Ser Asp Asp 546 ATT GAG AAG AGG AAA CGT CAG CGC CAA AAG AAG GCT CGG GAG 2378 Ile Glu Lys Arg Lys Arg Gln Arg Gln Lys Lys Ala Arg Glu 560 GAA CGC CGC CGA GAG CGC AGG ATT GAG ATA GAG GAG AAC AAG 2420 Glu Arg Arg Glu Arg Arg Ile Glu Ile Glu Glu Asn Lys 574 AAA CAG GGC AAG TAC CCA GAA GTC CAC ATT CCC CTC GAG AAT 2462 Lys Gln Gly Lys Tyr Pro Glu Val His Ile Pro Leu Glu Asn 588

GCC TTC AAT TCT TAT ACC TG CTA CAG CAG TTT Leu Gln Gln Phe Pro Ala Phe Asn Ser Tyr Thr Cys Ser Ser 602 GAT TCT GCT TTG GGT CCC ACC AGC ACC GAG GGC CAT GGG GCC 2546 Asp Ser Ala Leu Gly Pro Thr Ser Thr Glu Gly His Gly Ala 616 CTC TCC ATT TCT CCT CTC AGC AGA AGT CCA GGT TCC CAT GCA 2588 Leu Ser Ile Ser Pro Leu Ser Arg Ser Pro Gly Ser His Ala 630 GAC TTT CTG CTG ACC CCT CTG TCA CCC ACT GCC AGT CAG GGC 2630 Asp Phe Leu Leu Thr Pro Leu Ser Pro Thr Ala Ser Gln Gly 644 AGT CCC TCA TTC TGC GTT GGG AGT CTG GAA GAA GAC TCT CCC 2672 . Ser Pro Ser Phe Cys Val Gly Ser Leu Glu Glu Asp Ser Pro 658 TTC CCT TCC TTT GCC CAG ATG CTG AGG GTT GGA AAA GCA AAA 2714 Phe Pro Ser Phe Ala Gln Met Leu Arg Val Gly Lys Ala Lys 672 GCA GAT GTG TGG CCC AAA ACT GCT CCA AAG AAA GAT GAG AAC 2756 Ala Asp Val Trp Pro Lys Thr Ala Pro Lys Lys Asp Glu Asn 686 AGC TTA GTT CCT CCT GCC CCT GTG GAC AGC GAC GGG GAG AGT 2798 Ser Leu Val Pro Pro Ala Pro Val Asp Ser Asp Gly Glu Ser 700 GAT AAT TCA GAC CGT GTT CCT GTG CCC AGT TTT CAA AAT TCC 2840 Asp Asn Ser Asp Arg Val Pro Val Pro Ser Phe Gln Asn Ser 714 TTC AGC CAA GCT ATT GAA GCA GCC TTC ATG AAA CTG GAC ACA 2882 Phe Ser Gln Ala Ile Glu Ala Ala Phe Met Lys Leu Asp Thr 728 CCA GCT ACT TCA GAT CCC CTC TCT GAA GAG AAA GGA AAG 2924 Pro Ala Thr Ser Asp Pro Leu Ser Glu Glu Lys Gly Gly Lys 742 AAA AGA AAA AAA CAG AAA CAG AAG CTC CTG TTC AGC ACC TCA 2966 Lys Arg Lys Lys Gln Lys Gln Lys Leu Leu Phe Ser Thr Ser 756 GTC GTC CAC ACC AAG TGA CACTACTGG CCCAGGCTAC CTTCTCCATC 3013 761 Val Val His Thr Lys Stop TGGTTTTTGT TTTTGTTTTT TTTTCCCCCA TGCTTTTGTT TGGCTGCTGT 3063 AATTTTTAAG TATTTGAGTT TGAACAGATT AGCTCTGGGG GGAGGGGGTT 3113 TCCACAATGT GAGGGGGAAC CAAGAAAATT TTAAATACAG TGTATTTTCC 3163 3205 AGCTTCCTGT CTTTACACCA AAATAAAGTA TTGACACAAG AG







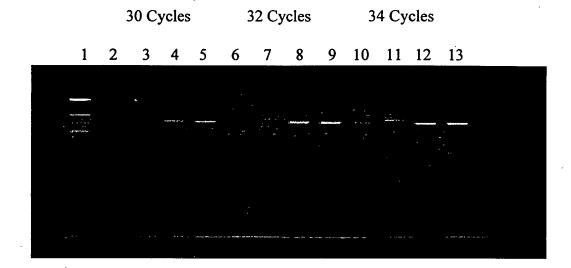


FIG. 14

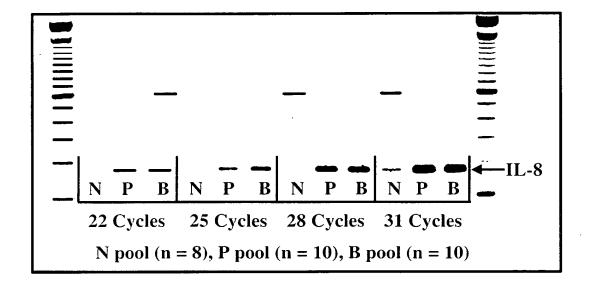


FIG. 1A

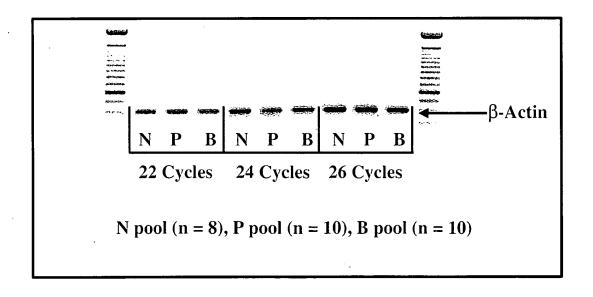


FIG. 1B

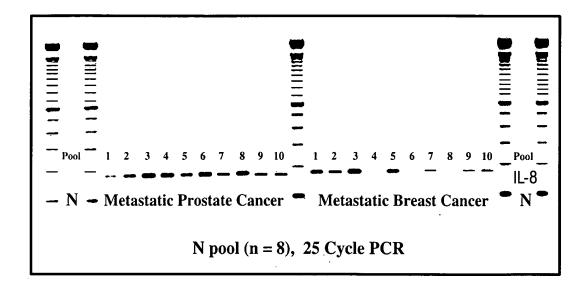
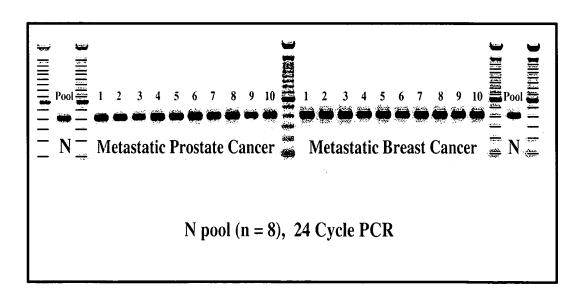


FIG. 2A



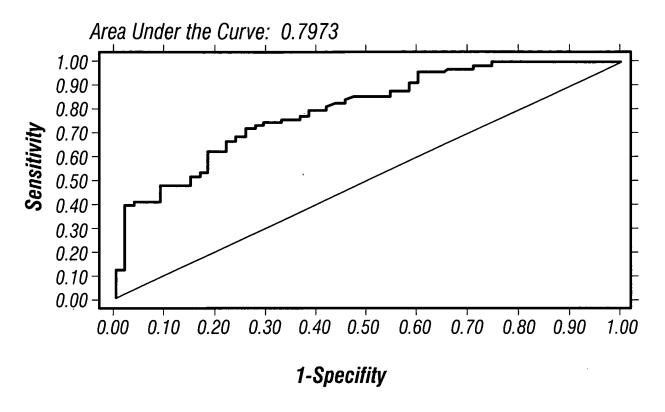


FIG. 3

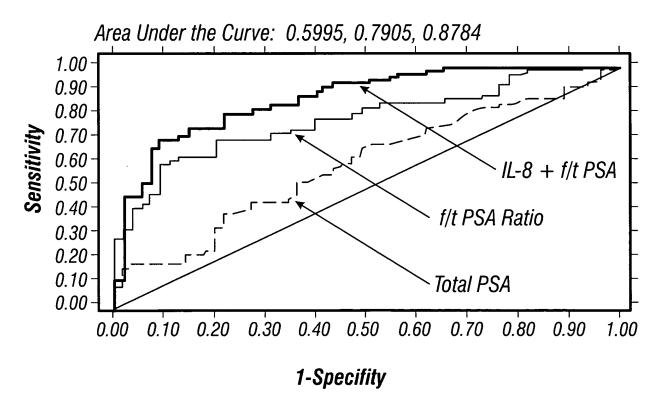
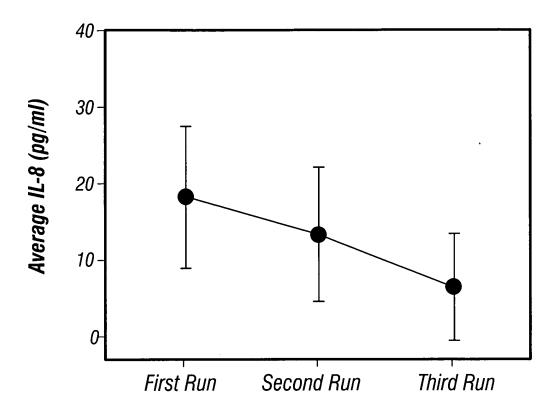


FIG. 4



Freeze/Thaw Sample Sequence

FIG. 5

HUM-UC33 HUM-UC33 MOU-UC33	TACGGGCAATGTCAAGGCATCATTATAATGGGAGAGATGATGACTCACACCC TACGGGCAATGTCAAAGGCGTCATCATAATGGGAGGATGATGACTCACACCC *	390 390 3CAATGTCAAGCTCAAAGGCATCATTZ 3CAATGTCAAGCTGAAAGGCGTCATCZ
	42(ATAATGGGAGGATGATGACTCACACC ATAATGGGCGAGGATGATGACTCGCACC	390 STCAAGCTCAAAGGCATCATTA STCAAGCTGAAAGGCGTCATCA
0 T HUM-UC331 T MOU-UC331	330 CGACCGCTCCAAGTTTATTGAAAGTGATGCAGATGAAGAGCTTCTGTTTAATATTTCCATT CGACCGCTCCAAGTTCGCTGAAGTGATGCGGACGAAGAGCTCCTGTTTAATATTTCCGTT * * * * * * * * * *	330 CGACCGCTCCAAGTTTATTGAAAGTGATGCAC CGACCGCTCCAAGTTCGCTGAAAGTGATGCGC
C HUM-UC331 C MOU-UC331	CCTTAACGAGAGCCGCGAGCGGCCGCGCGCGTCTTCAAGCCATGGGAGGGA	AGCCGCGAGGCAGCGGCCGCC
G HUM-UC331 0	240 CTGTACCTGCATCGACCTGGAGCGCTGCAATG 270	ZIO CGAGCAGCGGCCTGGCCTACGGCCTGTACC 270
0 C HUM-UC331	180 GCACGGTCACAGCCACGGGGGGGGGTGGCTGCCGCTGCGCCGCCGAACGGGAGGAGCCGCC	150 AGCCACGGGGGGGTGGCTGCC
C HUM-UC331	CCGAGAGGACGCGCGGCGCGTTGCC <u>ATG</u> TC START	CAAGCGAGCGCGCGATAGGGGCCGAGAC
	120	

		, ,	, ,		, ,
HUM-UC331 MOU-UC331	HUM-UC331 MOU-UC331	HUM-UC331 MOU-UC331	HUM-UC331 MOU-UC331	HUM-UC331 MOU-UC331	HUM-UC331 MOU-UC331
870 AGTIGGCIGCCACAGCICIG-CCAAGCITIGICITITGGGGCTIGCTGCAGAAACCIGGCC AGIIGCCIGCCAGAGCITIGGCCAGGCITITGIC-ICGGGG-IIGCIGCAGGAACCIGGCC * * * * * *	930 FACGGAAGATACGACACCACTGGGAGGGTTGTGTAGGTGCCAGGGGACCATCGTGGTTCT FGTGGAAACCGCCTCACCACGGAGCGGTATGGGTGCCAAGGGATAGTCTCTCT ** *** ** ** ** ** ** ***	1020 CTAGGGCGCTGTGGAAATTGGGTCTTGGGCTGGGTGGCATCTGGCAGTCATGGGTAACAC CTAAGGCACTGCAGAAACTGGGTCTTAGGCTGGGTGGCATCTGTCAGTCA	1080 FIGCTITITCCAGTTAATGTGGCCATGTGATTCCAAGTGTCATGTTGCTTTGTGGAAGATT FCACTT-CCCAGTCTGTGGCCACGGGATCCCATGTGTCTTTTTGCTT-GATTTCTTGT ** ** ** *************************	1110 STTGTGTGTCTTTTTTTTTGTTTTTTGTTTTTTTTAAAGGAAACTATTTGTGGGC STGGTTTGTCCT-TTTGTGCATCAAAAAGGATGCTTCCTTGACCG * * * * * * * * * * * * * * * * * * *	1170 IATAGGAAACTTTCTGATGCCTCCGGATT-GTGTTAGTAGTAGCCATCAGGAGGGTCTCC FAGAATCCTTCTGAAACCCG-AGTTTCGTGTTTGAATTAGCCATCAGGAGGGTCTCC * **** * * * * * * * * * * * * * * *

HUM-UC331	HUM-UC331	HUM-UC331	HUM-UC331	HUM-UC331	HUM-UC331
MOU-UC331	MOU-UC331	MOU-UC331	MOU-UC331	MOU-UC331	MOU-UC331
HUM	HUM	HUM	HUM	HUM	HUM
MOU	MOU	MOU	MOU	MOU	MOU
1230 AACTA-AAACACTT-GTTCCTGCTTGCTCCTTTTCCCCTCTCATTGTTCAGCATTCTTGTC HI AGCTAGAAACACTTCGTCCTGCTTGCTCCT-CCTCCTGTCATTGCTCAGCATTCGTGTC MC * * * * * * * * * * * * * * * * * * *	1290 AAGTTGCCCAGCTTGGAGTTGTCTGTCACGCACATGTGTCCTGTGGTTATAGCTAGAAGG HI AGGGTGCCTAGCT-GGTGTCACATATCAGACACAAGTGTCCCACAATGGTGGTTGGAAAG MC * * * * * * * * * * * * * * * * * * *	ACAGGAGTCTCCTGCTGATGCGTGATAGCTTAAGCTTGGGGAGAAGGTCTTTTCCACTGC HI GAAGGAGTCTCCTGATACATGACTGCTTGGGGAAGG-CTTACACAGT-C MC	1410 CTAAGCAGTCTGGGGAGAGCATGGGGATCATTTCTATGTGTGTG	1470 AGTAAGATTGAGACTTAAGATTCCCCTTGGAAATTCCTTAATGTTTATTAGCTT HI GGGGTAAAACTGAGACAGTAAAGATTCCTCTTGGGACCTCCTTGGTGTTTCCCTGCTT MC * ** * * * * * * * * * * * * * * * * *	1530 CTAACTAGTGTTGTAAGTCCGATGCCAGAATTTGGAGATTTGAGTTCTTCTTTTTCATGGC HI CTAACTCATGTTATAAACCCAGGGCTGGAGTCTGGAGACCCTGCTCTTCTTTTATGGC MC ** ** ** ** ** ** ** ** ** ** ** ** **
AACTA	AAGTT	ACAGG	CTAGC	AGT	CTAAC
AGCTA	AGGGT	GAAGG	TAGCC	GGGGT	
*	* *	**	****	* **	

	HUM-UC331	MOU-UC331	
1620	TITIAITCACTGTGACTAATAAGCTTCCTAATAAATCCTTGCCAGACTTAAAAAAAA	CCTTAG-AGACTTAAAA	*
1590	ACTAATAAGCTTCCTAATAAAT	TTTCATTCATGGTGACTAATGAGCTTCCTAATAAATCCTTAG-AGACTTAAAA	*
	CACTGTG	CATGGTG	*
	TTTTATI	TTTCATI	*

10 20 30 40 MSHGHSHGGGGCRCAAER-EEPPEORGLAYGLYLRIDLE HUM-UC331 >CSHGHSHN-----CAAEHIPEVPGDDVYRYDMVSYIDME ZK353.1 50 60 70 80 RLOCLNESREGSGRGVFKPWEERTDRSKFIESDADEELLF HUM-UC331 >FKPWEERTDRSKFAESDADEELLF MOU-UC331 KVTTLNESVDGAGKKVFKVMEKRDDRLEYVESDCDHELLF ZK353.1 90 100 110 120 NIPFTGNVKLKGIIIMGEDDDSHPSEMRLYKNIPOMSFDD HUM-UC331 NIPFTCNVKLKGVIIMGEDDDSHPSEMRLYKNIPOMSFDD MOU-UC331 NIPFTGHVRLTGLSIIGDEDGSHPAKIRLFKDREAMSFDD ZK353.1 130 140 150 160 TEREPDOTFSLNRDLTGELEYATKISRFSNVYHLSIHISK HUM-UC331 TEREPEOTFSLNRDITGELEYATKISRFSNVYHLSIHISK MOU-UC331 CSIEADOEIDLKODPOGLVDYPLKASKFGNIHNLSILVDA ZK353.1 170 180 190 200 NFGADTTKVFYIGLRGEWTELRRHEVTICNYEASANPADH HUM-UC331 NFGADTTKIFYIGLRGEWTELRRHEVTICNYEASANPADH MOU-UC331 NFGEDETKIYYIGLRGEFQHEFRQRIAIATYESRAQLKDH ZK353.1

210

RVHQVTPQTHFIS. HUM-UC331 RVHQVTPQTHFIS. MOU-UC331 KNEIPDAVAKGLF. ZK353.1

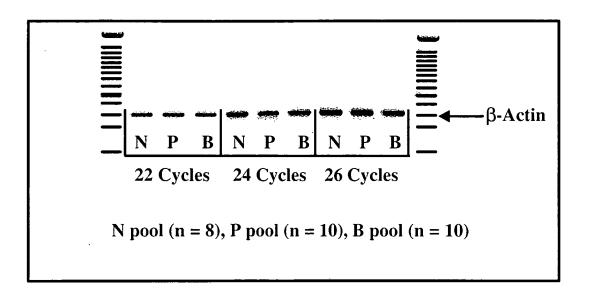


FIG. 8A

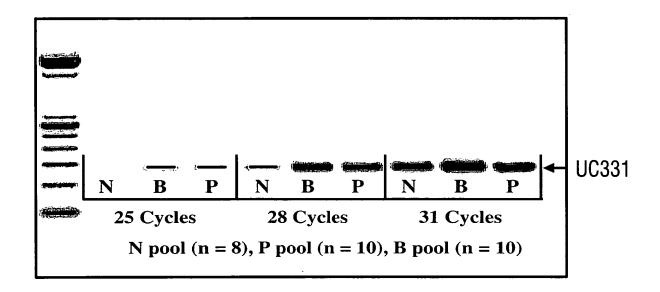


FIG. 8B

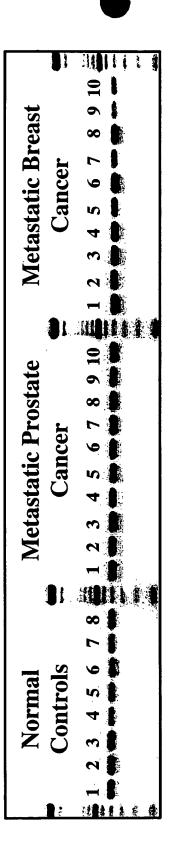


FIG. 9A

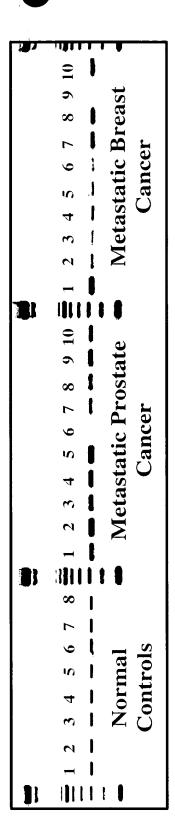


FIG. 9B

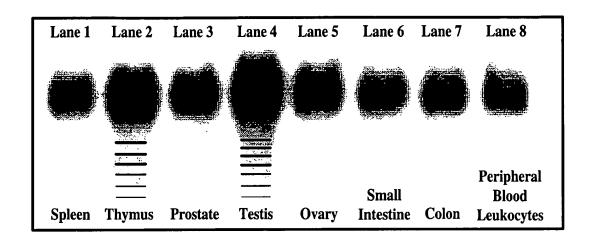


FIG. 10

50	GGGCGAGTA	100	CAGCCAGCCC	150	9990990099	200	ದರಿದಿದ್ದರು	250	CGGTCGCCGC	300	TAGTTTGAGA	350	CGAGAACCGC	400	TGGGTCCCCG	450	CCCGTTGATG	200	TGGACAAGAA	550	AAAGGGCAAC	009	TAAACCCAAG
40	CCTCGGCCCA	06	GACACCGAGA	140	ವಿದಿರಿದಿದಿದಿದಿದ	190	CCCGCAGCCT	240	TCCTCGTCCT	290	CTTCTCTTCC	340	CCATGAAGGC	390	GCCATGAGCC	440	CGCCGAGGCC	490	GCCTCCGACA	540	GGGCAGCAGC	590	CCGGCGAGTC
30	AGCAGGTCGG	80	ACTAGTCCCC	130	GAGAGCGTGT	180	CICCCCIICC	230	AGCCCCGGCC	280	CCGICCGCCG	330	AAAAATGTCG	380	GGCCCTGAAC	430	CIGCCGICGC	480	CGCCGCCACC	530	CCGCCTCTTC	580	GCGGGGCCAG
20	CCATTCCCGG	70	TGTCGGAGAC	120	CTCGCGGCGG	170	CCICCCICGC	220	CGGACTCCCG	270	CTTAACAGCC	320	GGAAACAGGG	370	GACCCCCGCC	420	TCCGCTCCGA	470	CCCCCAACGC	520	AACAGCTCCT	570	CICCGCCICG
10	CGACTCGTCG	09	TCCGTTGCTG	110	TCTCCCCTGC	160	GCTCGCGCAA	210	AGGCCCGGCC	260	TGCCGCCGGG	310	AGCCAAGGAA	360	TGCCGCCGCC	410	ದಿರಿದಿದ್ದಾರು	460	CCGCTGAGCT	510	CAGCGGCTCC	260	AGCCGCCCCG

	740 14	782 28	824 42	866 56	908	950 84	992 98
50 GT	AAT '	AAC '	TTT 8	CTC (GCA 9	GGT G	TTT Phe
650 TTGATTCTGT 698 TACTCTGG	TAT	TTT Phe	ACT Thr	AAA	GTA Val	TCT (ACT
6 TTGATTCT 698 TACTCTGG	CGT Arg	AGT Ser	AAG Lys	AGC	GAG Glu	TTC Phe	TTC
640 CAG 690 AAC	AAG Lys	GAA Glu	AGC Ser	AGC Ser	GAT Asp	CAG Gln	AAT Asn
640 TTGTTGTCAG 690 GCTTGTCAAC	TCC Ser	AAT Asn	AAA Lys	GGC Gly	CGA Arg	GCC Ala	TTG
	GGA	AAA Lys	CAG Gln	GGC Gly	AGA Arg	CCT Pro	TTG Leu
630 CAAT 680 AGGT	AGT Ser	CCC Pro	TCA Ser	GGC	GGA Gly	AGC Ser	CAC His
630 TGGATTCAAT 680 CTCTGGAGGT	TCC Ser	\mathtt{TAC}	AGT Ser	AGG Arg	GGT	TTT Phe	AAC Asn
	AAC Asn	TCC Ser	TCC Ser	CAA Gln	AAT Asn	GAG Glu	CTG Leu
620 TAATTTCAGC 670 TATGTTGCCC	AAG Lys	CTT Leu	CGC Arg	CCT Pro	TTT Phe	GCA Ala	AAC Asn
'AATT	GGA Gly	GAA Glu	CGT Arg	CCT Pro	TCT Ser	CGG	ATC
	GAT Asp	CGT Arg	TCC Ser	ATG Met	TCT Ser	CAA CGG Gln Arg	AAG Lys
610 AGCGAATTAC 660 AGTAAGGCCA	ATG Met	AAA Lys	CAG Gln	AAG Lys	AGC Ser	GCT Ala	AAG AAG Lys Lys
AGCG	ATG Met	CGC Arg	AAC Asn	AAC Asn	TTT Phe	GAG Glu	CCT Pro

1034	1076 126	1118 140	1160 154	1202 168	1244	1286 196	1328 210
CAT His	TTT Phe	GTG Val	GAT Asp	${\tt TGT} \\ {\tt CYS}$	CCT	TGG	
GGA Gly	CCT	GTG Val	CCT	ATT Ile	CCA	TGC	ACG
AGT Ser	AAG Lys	TTT Phe	GAT Asp	CGC Arg	TAT	TTC	AAG Lvs
GGC Gly	CAT His	CAA Gln	GCT Ala	GTG Val	CTC	ATC	CTT TCA CTG AGT GAG AAG ACG TGG Leu Ser Leu Ser Glu Lys Thr Trp
GAA Glu	GGA Gly	TGC Cys	TTT Phe	CAA Gln	TGC	CAC	AGT
TTT Phe	TGG Trp	AAC Asn	CAT His	GAA Glu	ATA	GGA Gly	CTG
CAC His	AAG Lys	GCC Ala	GCT Ala	GTG Val	CCA	TGT	TCA
\mathtt{GGT}	AAC Asn	CAG Gln	ACA Thr	TTT Phe	TGC	CGT	CTT
ACG Thr	AGG Arg	TTA Leu	$\mathtt{TAC}\\ \mathtt{TY} r$	GAC Asp	TCT	ACC Thr	TAT
CAG Gln	AAG Lys	TTT Phe	GAC Asp	TGG Trp	CCA Pro	ATA	CAC
GGC Gly	GGA Gly	CTC	CAA Gln	AAC Asn	GTG Val	AAG	ATC CTG Ile Leu
CGT Arg	TGG Trp	GAA Glu	GAC Asp	GTT Val	GAA Glu	GCC	TGC ATC CTG Cvs Ile Leu
CCC Pro	AGC Ser	AAG Lys	GAA Glu	TTA Leu	CAT His	GCA	TGC
saa slu	3GT	AAC Asn	CT	\CA lhr	AGC Ser	\CT lhr	3CA 11a

0	
137	224
GAT	Asp
AAG	Lys
AAG	Lys
CAT	His
GIG	Val
$_{ m LCL}$	Ser
AGT	Ser
TAC] Tyr
\mathtt{TGT}	Cys
ATC TGT	Ile
CCC	Pro
\mathtt{TGT}	Cys
AAA	Ser Lys Cys
AGT	Ser

1412	238
GTT	Val
\mathtt{GLL}	Val
\mathtt{TAT}	Tyr
CAG	Gln
CAT	His
TCA	Ser
GAG	Glu
ACA	\mathtt{Thr}
GCC	Ala
$_{ m GLL}$	Val
GLL	Val
AGT	Ser
AAG	Lys
CIC	Leu

1538	280
$_{ m LCC}$	Ser
TAC	Tyr
CAG	Gln
AGC	Ser
CAC	His
CAG	Gln
GAA	Glu
GAT	Asp
GGA	Gly
CTA	Leu
CAT	His
ATT	Ile
CCC	Pro
CAT	His

1622	308
GAG	Glu
GCA	Ala
CIG	Leu
CAG	Gln
CAG	Gln
GAG	Glu
CTA	Leu
GCA	Ala
\mathtt{GTA}	Val
AAA	Lys
GAG	Glu
GAG	Glu
CTG	Leu
GTT	Val

664	322
ATC 1664	
	a Ile
GCT	Ala
GCA	Ala
GAG	Glu
ATT	Ile
LLL	Phe
TGC	CVS
ICC	Ser
GAG	Glu
CCC	Pro
ACT	Thr
CAC	His
AAG	LVS
GAG	Glu

1706 336 gaa Ala TTGLeu G1yGGA TCG Ser Leu CIG Ala GCT Glu GAG Glu GAA Arg CGG Thr ACT AAG LysCIC Len Glu GAG CAG Gln

1748 350 GAA Glu Leu CIG GCT Ala GCT Ala GIG Val GTT Val G1yGGT ACT \mathtt{Thr} GIC Val Glu GAG AGG Arg AGA Arg AGC Ser GGA G1y

1790 364 Phe TTTGTT Val TCTSer GAG Glu AAG Lys GCG Ala TIG Leu Pro CCC GCT Ala ATG Met Leu CIG GTG Val CIG Leu CAA Gln 1832 378 Asp GAT $_{
m LLC}$ Phe GCC Ala $_{\rm ICI}$ Ser CIG Len TAT TyrGAG CIG Leu Val GTG GGT Gly AAG Lys AGG Arg CCC Pro CAA Gln

1874 392 Arg AGA $_{
m LCI}$ Ser Pro CCI Thr ACT GAC Asp CIG Leu $_{\rm ICI}$ Ser IGI Cys GLL Val GAA GluACG Thr ACC Thr Glu GAA GAA Glu

1916 406 TCTSer GTG Val GCA Ala Glu GAA GAG Glu GAG Glu GAA Glu GTA Val CTG Leu Pro CCT CIC Len GCT Ala Leu CTT Pro CCT

1958 420 TTGLeu Asp GAC GATAsp $_{\mathrm{IGI}}$ Cys gaa Ala GAG Glu CCA Pro $_{
m TTG}$ Leu <u>ტტტ</u> GlyGAG Glu CCIPro GAG Glu CCA Pro GAA Glu

2000 ACT Thr $_{
m LGC}$ Cys ATT ACC Thr GGG Gly GAG Glu AAA Lys CTTLen AAT Asn Asp GAC Asp GAT Ala GCA Len TTA GAG Glu

2042 448	2084 462	2126 476	2168 490	2210 504	2252 518	2294 532	2336 546
ACA Thr	GAA Glu	TGC Cys	AAG Lys	TCT Ser	CCA Pro	CCT	GAC Asp
\mathtt{TTC}	GCG Ala	CGC Arg	GAG	ATG Met	TTG Leu	CAA Gln	GAT Asp
GGC Gly	CAA Gln	GTG Val	CCC	TCC Ser	CAC His	TTG Leu	TCA Ser
TCA Ser	\mathtt{TAC}	AAT Asn	AGC	\mathtt{TAC}	TCT Ser	GCT Ala	TTC Phe
\mathtt{AAG}	TTT Phe	GTG Val	AGG Arg	GGC Gly	CTC Leu	CTG Leu	ATG
ACC Thr	\mathtt{TAC}	CCT Pro	GAG Glu	GCT Ala	\mathtt{TAT}	GAA Glu	GAG Glu
ATC Ile	\mathtt{TAC}	CAC His	CTG	ATT	AGA Arg	TGT Cys	CTA Leu
CCC Pro	TGT Cys	CTG Leu	AGC	GAG	CAC His	ATC Ile	ACC Thr
GAA Glu	CCT	TTC Phe	GGC G1y	GTG	CGT Arg	AGC Ser	GAA Glu
CAG Gln	TCT Ser	ATG Met	TAC	GTG	CAG Gln	TTC Phe	AAG Lys
CAG Gln	AGC Ser	CAT His	GAG	ACT Thr	CGA Arg	GAG Glu	TCT
AGC Ser	AGC Ser	CAG Gln	CGG	TCA GCA Ser Ala	GTT Val	TGT Cys	GTC Val
TCC	CTC	$\texttt{GGA}\\ \texttt{G1}\underline{\texttt{y}}$	GTG Val	1 1	GAT GTT Asp Val	ACC Thr	GTG Val
GAG Glu	CGC Arg	GAT Asp	CTC	ATC Ile	GAG Glu	CTC	CCT

2420 2462 2546 2588 2378 2504 588 616 560 574 LysAAG TCTGCC GCA GAG Glu AAT Ser Ala Asn CGG Ard AAC Asn $_{\rm ICC}$ GGG G1yGlu Ser GAG CAT GAG Glu $_{
m LGC}$ GCT His $_{
m LCC}$ Ala CIC Leu CAT CysPro AAG GlyLysCCC ACC Thr GGIGAG Glu GGC AAG Ile GAG CCA LysATA Ile Glu TAT TyrATT CAA Gln Glu GAG ACC CAC Thr His $_{
m LCI}$ Ser AGT AGC CGC Ard Ser AGA Ile GIC AAT Asn ATT Val AGG $_{
m LLC}$ ACC CAG Arg GAA Glu Phe Thr AGC Gln Ard CGC Pro GCC Ala CCC Pro CTCCGI Arg CCA AAA GAG LysPro Glu TAC TyrCCIGGTGlyCCIAGG Arg TTGCGC CGA Ard TTTPhe Leu AAG LysTCT AAG $\overline{\text{Lys}}$ G1yCAG GCT Ala GGC Gln Arq ATT CGC GAG Glu Gln CAG CAG Gln $_{
m LCI}$ JCC Ser Ard ATT Asp GAA AAA CIC CTA GAT Glu LysLen

2672 658 CCC Pro $_{
m LCL}$ Ser Asp GAC GAA Glu GAA Glu CIG Len AGT Ser GGG Gly GTT Val LGC Cys TTCPhe TCA Ser CCC Pro AGT Ser

2630

GGC

CAG Gln

AGT

GCC

ACT

CCC

TCA

CIG

CCT

ACC

CTG

CIG

TTT

GAC

644

Gly

Ser

Ala

Pro

Ser

Leu

Thr

Len

Len

Phe

Asp

630

Ala

His

Ser

G1y

Pro

Ser

Arg

Ser

Len

Pro

Ser

Ile

Ser

Leu

	9	ω.	0	01	-41	9	m
2714 672	2756	2798 700	284(714	2882 728	2924 742	2966 756	3013
AAA Lys	AAC Asn	AGT	TCC	ACA Th <u>r</u>	AAG Lys	TCA Ser	ATC
GCA Ala	GAG Glu	GAG Glu	AAT Asn	GAC	${\tt GGA} \\ {\tt Gly}$	ACC Thr	CTTCTCCATC
AAA Lys	GAT	GGG G1y	CAA AAT Gln Asn	CTG	GGA Gly	AGC Ser	
GGA Gly	AAA Lys	GAC Asp	TTT Phe	TTC ATG AAA CTG GAC Phe Met Lys Leu Asp	AAA Lys	TTC Phe	CCCAGGCTAC
GTT Val	AAG Lys	AGC Ser	AGT Ser	ATG Met	GAG Glu	CTG Leu	CAGG
AGG Arg	CCA Pro	GAC Asp	CCC	TTC	GAA Glu	CTC Leu	
CTG Leu	GCT Ala	GTG Val	GTG Val	GCC Ala	TCT	AAG Lys	CACTACTGG
ATG Met	ACT Thr	CCT	CCT	GAA GCA GCC Glu Ala Ala	CTC	CAG Gln	CACI
CAG Gln	AAA Lys	GCC Ala	GTT Val	GAA Glu	CCC Pro	AAA Lys	TGA Stop
GCC Ala	CCC Pro	CCT	CGT	ATT Ile	GAT Asp	CAG Gln	AAG Lys
TTT Phe	TGG Trp	CCT	GAC Asp	GCT Ala	TCA	AAA Lys	ACC Thr
TCC Ser	GTG Val	GTT Val	TCA GAC Ser Asp	CAA GCT Gln Ala	GCT ACT TCA Ala Thr Ser	AGA AAA AAA Arg Lys Lys	CAC His
CCT Pro	GAT Asp	TTA	AAT Asn	AGC Ser	GCT Ala		GTC Val
TC	3CA	AGC Ger	SAT	TC	CCA	AAA	grc 7al

3063	3113	3163	3205
TTGTTTTT TTTTCCCCCA TGCTTTTGTT TGGCTGCTGT 3063	TTTGAGTT TGAACACATT AGCTCTGGGG GGAGGGGGTT 3113	GGGGGAAC CAAGAAATT TTAAATACAG TGTATTTTCC 3163	AG
TGCTTTTGTT	AGCTCTGGGG	TTAAATACAG	TTGACACAAG
TTTTCCCCCA	TGAACACATT	CAAGAAAATT	AAATAAAGTA
	TATTTGAGTT	GAGGGGGAAC	CTTTACACCA AAATAAAGTA TTGACACAAG AG
TGGTTTTTGT TT	AATTTTTAAG TA	TCCACAATGT GA	AGCTTCCTGT

	(UC332)	(BRCA1)	(rpt-1)	(Traf5)	(HT2A)	(MAT1)	(rfp)	(bmi-1)	(CRZF)	(nen)
מ	TWSKCPIC	SPSQCPLC	GKGNCFVC	STRELNSVPICEVC	NGVRCPFC	GAGNCPEC	TINVSCPQC	TSKYCPIC	TKKTCPVC	GGGCCPLC
	HYLSLSEK TWSKCPI	KLLNOKK	NYESNRNTD	SIRELI	KLLASSI	LIFVR	RCWGTAE	RYLE	M	EQWRGV
ט	FCWACIL	FCKFCML	FCRACITI	FCQQCIR	ICROCLE	LCESCVD	ICCACLA	SCKTCIV	YHCK CVDE	CMCYDCAI
CH	CGHI	CDHI	CNHS	CGHR	HCGHT	VCGHT	CGHIN	O H H	CSHA	CGH
ט	CPICLYPPTAAKITR	CPICLELIKEPVSTK	CPICLELLKEPVSAD	CAFCHSVLHNPHOTG	CPICMESFTEE OIRPKLLH	CPRCKTTKYRNPSLKLMVNV	CPVCLQYFAEPMMLD	CVLOGGYFIDATTIE	CALCIDEYEDGDKLRILP	GLICKENPIDSVLYM

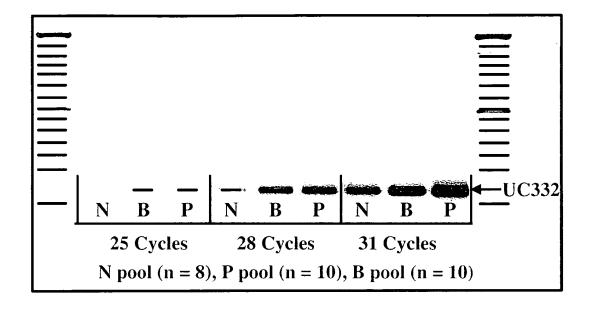


FIG. 13A

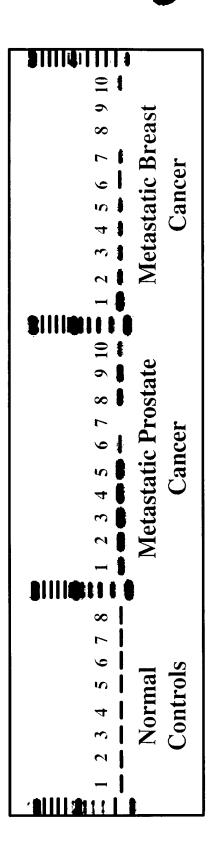


FIG. 13B

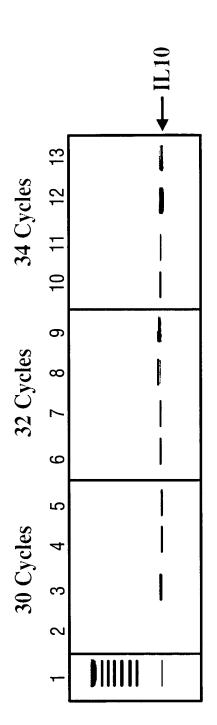


FIG. 14